

RAW SEQUENCE LISTING

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Application Serial Number: 10/552, 298
Source: PCT
Date Processed by STIC: 10/18/2005

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RAW SEQUENCE LISTING

DATE: 10/18/2005

PATENT APPLICATION: US/10/552,298

TIME: 10:10:33

Input Set : A:\034123-168 - Sequence Listing.txt

Output Set: N:\CRF4\10182005\J552298.raw

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3 <110> APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
4     GILL, Gordon N.
5     YEO, Michele
6     LIN, Patrick S.
7     DAHMUS, Michael E.
9 <120> TITLE OF INVENTION: PHOSPHATASE REGULATION OF NUCLEIC ACID TRANSCRIPTION
11 <130> FILE REFERENCE: UCSD1870WO
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/552,298
C--> 14 <141> CURRENT FILING DATE: 2005-09-30
16 <150> PRIOR APPLICATION NUMBER: US 60/459,786
17 <151> PRIOR FILING DATE: 2003-04-01
19 <160> NUMBER OF SEQ ID NOS: 67
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 783
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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31 ggcaaagggtg accagaagtc agcagcttcc cagaagcccc gaagccgggg catcctccac      120
33 tcactcttct gctgtgtctg ccgggatgat ggggaggccc tgctgtctca cagcggggcg      180
35 cccctgcttg tggaggagaa tggcgccatc cctaagacct cagtccaata cctgctccct      240
37 gaggccaagg cccaggactc agacaagatc tgcgtggtca tgcacctgga cgagacctg      300
39 gtgcacagct ccttcaagcc agtgaacaac gcgacttca tcatccctgt ggagattgat      360
41 ggggtggtcc accaggtcta cgtgttgaag cgctctcatg tggatgagtt cctgcagcga      420
43 atgggcgagc tctttgaatg tgtgctgttc actgctagcc tcgccaagta cgcagaccca      480
45 gtagctgacc tgctggacaa atggggggcc ttccggggcc ggctgtttcg agagtctgc      540
47 gtcttccacc gggggaacta cgtgaaggac ctgagccggt tgggtcgaga cctgcggcgg      600
49 gtgctcatcc tggacaattc acctgcctcc tatgtcttcc atccagacaa tgctgtaccg      660
51 gtggcctcgt ggtttgacaa catgagtgac acagagctcc acgacctcct ccccttcttc      720
53 gagcaactca gccgtgtgga cgacgtgtac tcagtgtctc ggcagccacg gccagggagc      780
55 tag
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59 <211> LENGTH: 260
60 <212> TYPE: PRT
61 <213> ORGANISM: Homo sapiens
63 <400> SEQUENCE: 2
65 Met Asp Ser Ser Ala Val Ile Thr Gln Ile Ser Lys Glu Glu Ala Arg
66 1             5             10             15
69 Gly Pro Leu Arg Gly Lys Gly Asp Gln Lys Ser Ala Ala Ser Gln Lys
70             20             25             30
73 Pro Arg Ser Arg Gly Ile Leu His Ser Leu Phe Cys Cys Val Cys Arg
74             35             40             45

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77 Asp Asp Gly Glu Ala Leu Pro Ala His Ser Gly Ala Pro Leu Leu Val
78      50                      55                      60
81 Glu Glu Asn Gly Ala Ile Pro Lys Thr Pro Val Gln Tyr Leu Leu Pro
82 65                      70                      75                      80
85 Glu Ala Lys Ala Gln Asp Ser Asp Lys Ile Cys Val Val Ile Asp Leu
86      85                      90                      95
89 Asp Glu Thr Leu Val His Ser Ser Phe Lys Pro Val Asn Asn Ala Asp
90      100                      105                      110
93 Phe Ile Ile Pro Val Glu Ile Asp Gly Val Val His Gln Val Tyr Val
94      115                      120                      125
97 Leu Lys Arg Pro His Val Asp Glu Phe Leu Gln Arg Met Gly Glu Leu
98      130                      135                      140
101 Phe Glu Cys Val Leu Phe Thr Ala Ser Leu Ala Lys Tyr Ala Asp Pro
102 145                      150                      155                      160
105 Val Ala Asp Leu Leu Asp Lys Trp Gly Ala Phe Arg Ala Arg Leu Phe
106      165                      170                      175
109 Arg Glu Ser Cys Val Phe His Arg Gly Asn Tyr Val Lys Asp Leu Ser
110      180                      185                      190
113 Arg Leu Gly Arg Asp Leu Arg Arg Val Leu Ile Leu Asp Asn Ser Pro
114      195                      200                      205
117 Ala Ser Tyr Val Phe His Pro Asp Asn Ala Val Pro Val Ala Ser Trp
118      210                      215                      220
121 Phe Asp Asn Met Ser Asp Thr Glu Leu His Asp Leu Leu Pro Phe Phe
122 225                      230                      235                      240
125 Glu Gln Leu Ser Arg Val Asp Asp Val Tyr Ser Val Leu Arg Gln Pro
126      245                      250                      255
129 Arg Pro Gly Ser
130      260
133 <210> SEQ ID NO: 3
134 <211> LENGTH: 852
135 <212> TYPE: DNA
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 3
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141 caaggcctgg tctccaagtc ctctcctaag aagcctcgtg gacgtaacat cttcaaggcc      120
143 cttttctgct gttttcgcgc ccagcatggt ggccagtcaa gttcctccac tgagctcgct      180
145 gcgtataagg aggaagcaaa caccattgct aagtcggatc tgctccagtg tctccagtac      240
147 cagttctacc agatcccagg gacctgctcg ctcccagagg tgacagagga agatcaagga      300
149 aggatctgtg tggtcattga cctcgatgaa acccttgtgc atagctcctt taagccaatc      360
151 aacaatgctg acttcatagt gcctatagag attgagggga ccactcacca ggtgtatgtg      420
153 ctcaagaggc cttatgtgga tgagttcctg agacgcatgg gggaactctt tgaatgtgtt      480
155 ctcttcactg ccagcctggc caagtatgcc gacctgtga cagacctgct ggaccggtgt      540
157 ggggtgttcc gggcccgctt attccgtgag tcttgctgtt tccaccaggg ctgctacgtc      600
159 aaggacctca gccgcctggg gagggacctg agaaagaccc tcatcctgga caactcgcct      660
161 gcttcttaca tattccaccc cgagaatgca gtgcctgtgc agtcctggtt tgatgacatg      720
163 gcagacactg agttgctgaa cctgatccca atctttgagg agctgagcgg agcagaggac      780
165 gtctacacca gccttggggc agctgcgggc cccttagcct gccctgcttc caagcgacgg      840
167 ccacccagtg ag
170 <210> SEQ ID NO: 4

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171 <211> LENGTH: 283

172 <212> TYPE: PRT

173 <213> ORGANISM: Homo sapiens

175 <400> SEQUENCE: 4

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177 Met Glu His Gly Ser Ile Ile Thr Gln Ala Arg Arg Glu Asp Ala Leu
178 1          5          10          15
181 Val Leu Thr Lys Gln Gly Leu Val Ser Lys Ser Ser Pro Lys Lys Pro
182          20          25          30
185 Arg Gly Arg Asn Ile Phe Lys Ala Leu Phe Cys Cys Phe Arg Ala Gln
186          35          40          45
189 His Val Gly Gln Ser Ser Ser Ser Thr Glu Leu Ala Ala Tyr Lys Glu
190          50          55          60
193 Glu Ala Asn Thr Ile Ala Lys Ser Asp Leu Leu Gln Cys Leu Gln Tyr
194 65          70          75          80
197 Gln Phe Tyr Gln Ile Pro Gly Thr Cys Leu Leu Pro Glu Val Thr Glu
198          85          90          95
201 Glu Asp Gln Gly Arg Ile Cys Val Val Ile Asp Leu Asp Glu Thr Leu
202          100         105         110
205 Val His Ser Ser Phe Lys Pro Ile Asn Asn Ala Asp Phe Ile Val Pro
206          115         120         125
209 Ile Glu Ile Glu Gly Thr Thr His Gln Val Tyr Val Leu Lys Arg Pro
210          130         135         140
213 Tyr Val Asp Glu Phe Leu Arg Arg Met Gly Glu Leu Phe Glu Cys Val
214 145          150         155         160
217 Leu Phe Thr Ala Ser Leu Ala Lys Tyr Ala Asp Pro Val Thr Asp Leu
218          165         170         175
221 Leu Asp Arg Cys Gly Val Phe Arg Ala Arg Leu Phe Arg Glu Ser Cys
222          180         185         190
225 Val Phe His Gln Gly Cys Tyr Val Lys Asp Leu Ser Arg Leu Gly Arg
226          195         200         205
229 Asp Leu Arg Lys Thr Leu Ile Leu Asp Asn Ser Pro Ala Ser Tyr Ile
230          210         215         220
233 Phe His Pro Glu Asn Ala Val Pro Val Gln Ser Trp Phe Asp Asp Met
234 225          230         235         240
237 Ala Asp Thr Glu Leu Leu Asn Leu Ile Pro Ile Phe Glu Glu Leu Ser
238          245         250         255
241 Gly Ala Glu Asp Val Tyr Thr Ser Leu Gly Ala Ala Ala Gly Pro Leu
242          260         265         270
245 Ala Cys Pro Ala Ser Lys Arg Arg Pro Ser Gln
246          275         280

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249 <210> SEQ ID NO: 5

250 <211> LENGTH: 798

251 <212> TYPE: DNA

252 <213> ORGANISM: Homo sapiens

254 <400> SEQUENCE: 5

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257 ccgggcgcgg gcgagaaagc ctcccagtg aacgtcagct taaagaagca gaggagccgc      120
259 agcatcctta gctccttctt ctgctgcttc cgtgattaca atgtggaggc cctccaccc      180
261 agcagcccca gtgtgcttcc gccactggtg gaggagaatg gtgggcttca gaagccacca      240

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263 gctaagtacc ttcttccaga ggtgacggtg cttgactatg gaaagaaatg tgtgggcatt 300
265 gatttagatg aaacattggt gcacagttcg tttaagccta ttagtaatgc tgattttatt 360
267 gttccggttg aaatcgatgg aactatacat caggtgtatg tgctgaagcg gccacatgtg 420
269 gacgagttcc tccagaggat ggggcagctt tttgaatgtg tgctctttac tgccagcttg 480
271 gccaagtatg cagaccctgt ggctgacctc ctagaccgct ggggtgtgtt ccgggcccgg 540
273 ctcttcagag aatcatgtgt ttttcacgtt gggaactacg tgaaggacct gagtgcctt 600
275 gggcgggagc tgagcaaagt gatcattgtt gacaattccc ctgcctcata catcttccat 660
277 cctgagaatg cagtgcctgt gcagtcctgg ttcatgaca tgacggacac ggagctgctg 720
279 gacctcatcc cttcttttga gggcctgagc cgggaggacg acgtgtacag catgctgcac 780
281 agactctgca ataggtag 798
284 <210> SEQ ID NO: 6
285 <211> LENGTH: 265
286 <212> TYPE: PRT
287 <213> ORGANISM: Homo sapiens
289 <400> SEQUENCE: 6
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292 1 5 10 15
295 Glu Gly Arg Leu Pro Gly Ala Gly Glu Lys Ala Ser Gln Cys Asn Val
296 20 25 30
299 Ser Leu Lys Lys Gln Arg Ser Arg Ser Ile Leu Ser Ser Phe Phe Cys
300 35 40 45
303 Cys Phe Arg Asp Tyr Asn Val Glu Ala Pro Pro Pro Ser Ser Pro Ser
304 50 55 60
307 Val Leu Pro Pro Leu Val Glu Glu Asn Gly Gly Leu Gln Lys Pro Pro
308 65 70 75 80
311 Ala Lys Tyr Leu Leu Pro Glu Val Thr Val Leu Asp Tyr Gly Lys Lys
312 85 90 95
315 Cys Val Val Ile Asp Leu Asp Glu Thr Leu Val His Ser Ser Phe Lys
316 100 105 110
319 Pro Ile Ser Asn Ala Asp Phe Ile Val Pro Val Glu Ile Asp Gly Thr
320 115 120 125
323 Ile His Gln Val Tyr Val Leu Lys Arg Pro His Val Asp Glu Phe Leu
324 130 135 140
327 Gln Arg Met Gly Gln Leu Phe Glu Cys Val Leu Phe Thr Ala Ser Leu
328 145 150 155 160
331 Ala Lys Tyr Ala Asp Pro Val Ala Asp Leu Leu Asp Arg Trp Gly Val
332 165 170 175
335 Phe Arg Ala Arg Leu Phe Arg Glu Ser Cys Val Phe His Arg Gly Asn
336 180 185 190
339 Tyr Val Lys Asp Leu Ser Arg Leu Gly Arg Glu Leu Ser Lys Val Ile
340 195 200 205
343 Ile Val Asp Asn Ser Pro Ala Ser Tyr Ile Phe His Pro Glu Asn Ala
344 210 215 220
347 Val Pro Val Gln Ser Trp Phe Asp Asp Met Thr Asp Thr Glu Leu Leu
348 225 230 235 240
351 Asp Leu Ile Pro Phe Phe Glu Gly Leu Ser Arg Glu Asp Asp Val Tyr
352 245 250 255
355 Ser Met Leu His Arg Leu Cys Asn Arg
356 260 265

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367 ccacccctaa ggcagacccc agtccaatac ctgctccctg aggccaaggc ccaggactca      120
369 gacaagatct gcgtggatcat cgacctggac gagaccctgg tgcacagctc cttcaagcca      180
371 gtgaacaacg cggacttcat catccctgtg gagattgatg ggggtggcca ccaggctctac      240
373 gtgttgaagc gtcctcacgt ggatgagttc ctgcagcgaa tgggcgagct ctttgaatgt      300
375 gtgctgttca ctgctagcct cgccaagtac gcagaccag tagctgacct gctggacaaa      360
377 tggggggcct tccgggcccg gctgtttcga gagtcctgcg tcttccaccg ggggaactac      420
379 gtgaaggacc tgagccgggt gggtcgagac ctgcggcggg tgctcactct ggacaattca      480
381 cctgcctcct atgtcttcca tccagacaat gctgtaccgg tggcctcgtg gtttgacaac      540
383 atgagtgaca cagagctcca cgacctctc cccttcttcg agcaactcag ccgtgtggac      600
385 gacgtgtact cagtgtctcag gcagccacgg ccagggaact ag              642
388 <210> SEQ ID NO: 8
389 <211> LENGTH: 213
390 <212> TYPE: PRT
391 <213> ORGANISM: Homo sapiens
393 <400> SEQUENCE: 8
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400          20         25         30
403 Pro Glu Ala Lys Ala Gln Asp Ser Asp Lys Ile Cys Val Val Ile Asp
404          35         40         45
407 Leu Asp Glu Thr Leu Val His Ser Ser Phe Lys Pro Val Asn Asn Ala
408          50         55         60
411 Asp Phe Ile Ile Pro Val Glu Ile Asp Gly Val Val His Gln Val Tyr
412 65        70        75        80
415 Val Leu Lys Arg Pro His Val Asp Glu Phe Leu Gln Arg Met Gly Glu
416          85        90        95
419 Leu Phe Glu Cys Val Leu Phe Thr Ala Ser Leu Ala Lys Tyr Ala Asp
420         100       105       110
423 Pro Val Ala Asp Leu Leu Asp Lys Trp Gly Ala Phe Arg Ala Arg Leu
424         115       120       125
427 Phe Arg Glu Ser Cys Val Phe His Arg Gly Asn Tyr Val Lys Asp Leu
428         130       135       140
431 Ser Arg Leu Gly Arg Asp Leu Arg Arg Val Leu Ile Leu Asp Asn Ser
432 145       150       155       160
435 Pro Ala Ser Tyr Val Phe His Pro Asp Asn Ala Val Pro Val Ala Ser
436         165       170       175
439 Trp Phe Asp Asn Met Ser Asp Thr Glu Leu His Asp Leu Leu Pro Phe
440         180       185       190
443 Phe Glu Gln Leu Ser Arg Val Asp Asp Val Tyr Ser Val Leu Arg Gln
444         195       200       205
447 Pro Arg Pro Gly Ser
448         210

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date